



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Presta et al.

Appl. No. : 09/724,524

Filed : November 27, 2000

For : HUMAN TRK RECEPTORS  
AND NEUROTROPHIC  
FACTOR INHIBITORS

Examiner : Unknown

) Group Art Unit: 1642

) I hereby certify that this correspondence and all  
) marked attachments are being deposited with  
) the United States Postal Service as first-class  
) mail in an envelope addressed to: Assistant  
) Commissioner for Patents, Washington, D.C.  
) 20231, on

July 11, 2001

(Date)

Ginger R. Dreger, Reg. No. 33,055

SEQUENCE SUBMISSION STATEMENT

Assistant Commissioner for Patents  
Washington, D.C. 20231

Dear Sir:

This is in response to the Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures, mailed on May 22, 2001.

I hereby state that the amendments, made in accordance with 37 C.F.R. § 1.825(a), included herewith, are supported in the application and that the Sequence Listing does not include new matter.

I hereby state that the computer readable form, submitted in accordance with 37 C.F.R. § 1.825(b), is the same as the paper form of the Sequence Listing.

Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

Dated: July 11, 2001

By:

Ginger R. Dreger  
Registration No. 33,055  
Attorney of Record  
620 Newport Center Drive  
Sixteenth Floor  
Newport Beach, CA 92660  
(415) 954-4114



Sequence Listing

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Presta, Leonard G.  
Shelton, David L.  
Urfer, Roman

(ii) TITLE OF INVENTION: Human trk Receptors and Neurotrophic Factor Inhibitors

(iii) NUMBER OF SEQUENCES: 41

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Knobbe, Martens, Olson & Bear  
(B) STREET: 620 Newport Center Drive 16th Floor  
(C) CITY: Newport Beach  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 92660

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA

(A) APPLICATION NUMBER: 09/724,524  
(B) FILING DATE: 27-NOV-2000  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/156,923  
(B) FILING DATE: 18-SEP-1998  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/359,705  
(B) FILING DATE: 20-DEC-1994  
(C) CLASSIFICATION:

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/286846  
(B) FILING DATE: 10-AUG-1994

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/215139  
(B) FILING DATE: 18-MAR-1994

(ix) ATTORNEY/AGENT INFORMATION:

(A) NAME: Dreger, Ginger  
(B) REGISTRATION NUMBER: 33,055  
(C) REFERENCE/DOCKET NUMBER: GENENT.33CP2C2

(x) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 949/760-0404

(B) TELEFAX: 949/760-9502

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3194 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGAAGGTTTA AAGAAGAAGC CGCAAAGCGC AGGGAAGGCC TCCCGGCACG 50  
GGTGGGGGAA AGCGGCCGGT GCAGCGCGGG GACAGGCACT CGGGCTGGCA 100  
CTGGCTGCTA GGGATGTCGT CCTGGATAAG GTGGCATGGA CCCGCCATGG 150  
CGCGGCTCTG GGGCTTCTGC TGGCTGGTTG TGGGCTTCTG GAGGGCCGCT 200  
TTCGCCTGTC CCACGTCTCTG CAAATGCAGT GCCTCTCGGA TCTGGTGCAG 250  
CGACCCCTTCT CCTGGCATCG TGGCATTTCC GAGATTGGAG CCTAACAGTG 300  
TAGATCCTGA GAACATCACC GAAATTTTCA TCGCAAACCA GAAAAGGTTA 350  
GAAATCATCA ACGAAGATGA TGTTGAAGCT TATGTGGGAC TGAGAAATCT 400  
GACAATTGTG GATTCTGGAT TAAAATTTGT GGCTCATAAA GCATTTCTGA 450  
AAAACAGCAA CCTGCAGCAC ATCAATTTTA CCCGAAACAA ACTGACGAGT 500  
TTGTCTAGGA AACATTTCCG TCACCTTGAC TTGTCTGAAC TGATCCTGGT 550  
GGGCAATCCA TTTACATGCT CCTGTGACAT TATGTGGATC AAGACTCTCC 600  
AAGAGGCTAA ATCCAGTCCA GACACTCAGG ATTTGTACTG CCTGAATGAA 650  
AGCAGCAAGA ATATTCCCCT GGCAAACCTG CAGATACCCA ATTGTGGTTT 700  
GCCATCTGCA AATCTGGCCG CACCTAACCT CACTGTGGAG GAAGGAAAGT 750  
CTATCACATT ATCCTGTAGT GTGGCAGGTG ATCCGGTTCC TAATATGTAT 800  
TGGGATGTTG GTAACCTGGT TTCCAAACAT ATGAATGAAA CAAGCCACAC 850  
ACAGGGCTCC TTAAGGATAA CTAACATTTT ATCCGATGAC AGTGGGAAGC 900  
AGATCTCTTG TGTGGCGGAA AATCTTGTAG GAGAAGATCA AGATTCTGTC 950  
AACCTCACTG TGCATTTTGC ACCAACTATC ACATTTCTCG AATCTCCAAC 1000  
CTCAGACCAC CACTGGTGCA TTCCATTCAC TGTGAAAGGC AACCCAAAAC 1050

CAGCGCTTCA GTGGTTCTAT AACGGGGCAA TATTGAATGA GTCCAAATAC 1100  
 ATCTGTACTA AAATACATGT TACCAATCAC ACGGAGTACC ACGGCTGCCT 1150  
 CCAGCTGGAT AATCCCACTC ACATGAACAA TGGGGACTAC ACTCTAATAG 1200  
 CCAAGAATGA GTATGGGAAG GATGAGAAAC AGATTTCTGC TCACTTCATG 1250  
 GGCTGGCCTG GAATTGACGA TGGTGCAAAC CCAAATTATC CTGATGTAAT 1300  
 TTATGAAGAT TATGGAAGT CAGCGAATGA CATCGGGGAC ACCACGAACA 1350  
 GAAGTAATGA AATCCCTTCC ACAGACGTCA CTGATAAAAC CGGTCGGGAA 1400  
 CATCTCTCGG TCTATGCTGT GGTGGTGATT GCGTCTGTGG TGGGATTTTG 1450  
 CCTTTTGGA ATGCTGTTTC TGCTTAAGTT GGCAAGACAC TCCAAGTTTG 1500  
 GCATGAAAGG CCCAGCCTCC GTTATCAGCA ATGATGATGA CTCTGCCAGC 1550  
 CCACTCCATC ACATCTCCAA TGGGAGTAAC ACTCCATCTT CTTCGGAAGG 1600  
 TGGCCCAGAT GCTGTCATTA TTGGAATGAC CAAGATCCCT GTCATTGAAA 1650  
 ATCCCCAGTA CTTTGGCATC ACCAACAGTC AGCTCAAGCC AGACACATTT 1700  
 GTTCAGCACA TCAAGCGACA TAACATTGTT CTGAAAAGGG AGCTAGGCGA 1750  
 AGGAGCCTTT GGAAAAGTGT TCCTAGCTGA ATGCTATAAC CTCTGTCCTG 1800  
 AGCAGGACAA GATCTTGGTG GCAGTGAAGA CCCTGAAGGA TGCCAGTGAC 1850  
 AATGCACGCA AGGACTTCCA CCGTGAGGCC GAGCTCCTGA CCAACCTCCA 1900  
 GCATGAGCAC ATCGTCAAGT TCTATGGCGT CTGCGTGGAG GGCGACCCCC 1950  
 TCATCATGGT CTTTGAGTAC ATGAAGCATG GGGACCTCAA CAAGTTCCTC 2000  
 AGGGCACACG GCCCTGATGC CGTGCTGATG GCTGAGGGCA ACCCGCCCAC 2050  
 GGAAGTACG CAGTCGCAGA TGCTGCATAT AGCCCAGCAG ATCGCCGCGG 2100  
 GCATGGTCTA CCTGGCGTCC CAGCACTTCG TGCACCGCGA TTTGGCCACC 2150  
 AGGAACTGCC TGGTCGGGGA GAACTTGCTG GTGAAAATCG GGGACTTTGG 2200  
 GATGTCCCGG GACGTGTACA GCACTGACTA CTACAGGGTC GGTGGCCACA 2250  
 CAATGCTGCC CATTCGCTGG ATGCCTCCAG AGAGCATCAT GTACAGGAAA 2300  
 TTCACGACGG AAAGCGACGT CTGGAGCCTG GGGGTCGTGT TGTGGGAGAT 2350  
 TTTCACCTAT GGCAAACAGC CCTGGTACCA GCTGTCAAAC AATGAGGTGA 2400  
 TAGAGTGTAT CACTCAGGGC CGAGTCCTGC AGCGACCCCG CACGTGCCCC 2450  
 CAGGAGGTGT ATGAGCTGAT GCTGGGGTGC TGGCAGCGAG AGCCCCACAT 2500

GAGGAAGAAC ATCAAGGGCA TCCATACCCT CCTTCAGAAC TTGGCCAAGG 2550  
CATCTCCGGT CTACCTGGAC ATTCTAGGCT AGGGCCCTTT TCCCCAGACC 2600  
GATCCTTCCC AACGTACTCC TCAGACGGGC TGAGAGGATG AACATCTTTT 2650  
AACTGCCGCT GGAGGCCACC AAGCTGCTCT CCTTCACTCT GACAGTATTA 2700  
ACATCAAAGA CTCCGAGAAG CTCTCGAGGG AAGCAGTGTG TACTTCTTCA 2750  
TCCATAGACA CAGTATTGAC TTCTTTTGG CATTATCTCT TTCTCTCTTT 2800  
CCATCTCCCT TGGTTGTTCC TTTTCTTTT TTTAAATTTT CTTTTCTTC 2850  
TTTTTTTTCG TCTTCCCTGC TTCACGATTC TTACCCTTTC TTTTGAATCA 2900  
ATCTGGCTTC TGCATTACTA TTAACCTCTGC ATAGACAAAG GCCTTAACAA 2950  
ACGTAATTTG TTATATCAGC AGACACTCCA GTTTGCCAC CACAACTAAC 3000  
AATGCCTTGT TGTATTCTCG CCTTTGATGT GGATGAAAAA AAGGGAAAAAC 3050  
AAATATTTCA CTAAACTTT GTCACCTCTG CTGTACAGAT ATCGAGAGTT 3100  
TCTATGGATT CACTTCTATT TATTTATTAT TATTACTGTT CTTATTGTTT 3150  
TTGGATGGCT TAAGCCTGTG TATAAAAAA AAAAAAATC TAGA 3194

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Ser	Trp	Ile	Arg	Trp	His	Gly	Pro	Ala	Met	Ala	Arg	Leu
1				5					10					15
Trp	Gly	Phe	Cys	Trp	Leu	Val	Val	Gly	Phe	Trp	Arg	Ala	Ala	Phe
			20						25					30
Ala	Cys	Pro	Thr	Ser	Cys	Lys	Cys	Ser	Ala	Ser	Arg	Ile	Trp	Cys
			35						40					45
Ser	Asp	Pro	Ser	Pro	Gly	Ile	Val	Ala	Phe	Pro	Arg	Leu	Glu	Pro
			50						55					60
Asn	Ser	Val	Asp	Pro	Glu	Asn	Ile	Thr	Glu	Ile	Phe	Ile	Ala	Asn
			65						70					75
Gln	Lys	Arg	Leu	Glu	Ile	Ile	Asn	Glu	Asp	Asp	Val	Glu	Ala	Tyr
			80						85					90
Val	Gly	Leu	Arg	Asn	Leu	Thr	Ile	Val	Asp	Ser	Gly	Leu	Lys	Phe

				95					100					105				
Val	Ala	His	Lys	Ala 110	Phe	Leu	Lys	Asn	Ser 115	Asn	Leu	Gln	His	Ile 120				
Asn	Phe	Thr	Arg	Asn 125	Lys	Leu	Thr	Ser	Leu 130	Ser	Arg	Lys	His	Phe 135				
Arg	His	Leu	Asp	Leu 140	Ser	Glu	Leu	Ile	Leu 145	Val	Gly	Asn	Pro	Phe 150				
Thr	Cys	Ser	Cys	Asp 155	Ile	Met	Trp	Ile	Lys 160	Thr	Leu	Gln	Glu	Ala 165				
Lys	Ser	Ser	Pro	Asp 170	Thr	Gln	Asp	Leu	Tyr 175	Cys	Leu	Asn	Glu	Ser 180				
Ser	Lys	Asn	Ile	Pro 185	Leu	Ala	Asn	Leu	Gln 190	Ile	Pro	Asn	Cys	Gly 195				
Leu	Pro	Ser	Ala	Asn 200	Leu	Ala	Ala	Pro	Asn 205	Leu	Thr	Val	Glu	Glu 210				
Gly	Lys	Ser	Ile	Thr 215	Leu	Ser	Cys	Ser	Val 220	Ala	Gly	Asp	Pro	Val 225				
Pro	Asn	Met	Tyr	Trp 230	Asp	Val	Gly	Asn	Leu 235	Val	Ser	Lys	His	Met 240				
Asn	Glu	Thr	Ser	His 245	Thr	Gln	Gly	Ser	Leu 250	Arg	Ile	Thr	Asn	Ile 255				
Ser	Ser	Asp	Asp	Ser 260	Gly	Lys	Gln	Ile	Ser 265	Cys	Val	Ala	Glu	Asn 270				
Leu	Val	Gly	Glu	Asp 275	Gln	Asp	Ser	Val	Asn 280	Leu	Thr	Val	His	Phe 285				
Ala	Pro	Thr	Ile	Thr 290	Phe	Leu	Glu	Ser	Pro 295	Thr	Ser	Asp	His	His 300				
Trp	Cys	Ile	Pro	Phe 305	Thr	Val	Lys	Gly	Asn 310	Pro	Lys	Pro	Ala	Leu 315				
Gln	Trp	Phe	Tyr	Asn 320	Gly	Ala	Ile	Leu	Asn 325	Glu	Ser	Lys	Tyr	Ile 330				
Cys	Thr	Lys	Ile	His 335	Val	Thr	Asn	His	Thr 340	Glu	Tyr	His	Gly	Cys 345				
Leu	Gln	Leu	Asp	Asn 350	Pro	Thr	His	Met	Asn 355	Asn	Gly	Asp	Tyr	Thr 360				
Leu	Ile	Ala	Lys	Asn 365	Glu	Tyr	Gly	Lys	Asp 370	Glu	Lys	Gln	Ile	Ser 375				
Ala	His	Phe	Met	Gly	Trp	Pro	Gly	Ile	Asp	Asp	Gly	Ala	Asn	Pro				

380	385	390
Asn Tyr Pro Asp Val Ile Tyr Glu Asp Tyr Gly Thr Ala Ala Asn		
395	400	405
Asp Ile Gly Asp Thr Thr Asn Arg Ser Asn Glu Ile Pro Ser Thr		
410	415	420
Asp Val Thr Asp Lys Thr Gly Arg Glu His Leu Ser Val Tyr Ala		
425	430	435
Val Val Val Ile Ala Ser Val Val Gly Phe Cys Leu Leu Val Met		
440	445	450
Leu Phe Leu Leu Lys Leu Ala Arg His Ser Lys Phe Gly Met Lys		
455	460	465
Gly Pro Ala Ser Val Ile Ser Asn Asp Asp Asp Ser Ala Ser Pro		
470	475	480
Leu His His Ile Ser Asn Gly Ser Asn Thr Pro Ser Ser Ser Glu		
485	490	495
Gly Gly Pro Asp Ala Val Ile Ile Gly Met Thr Lys Ile Pro Val		
500	505	510
Ile Glu Asn Pro Gln Tyr Phe Gly Ile Thr Asn Ser Gln Leu Lys		
515	520	525
Pro Asp Thr Phe Val Gln His Ile Lys Arg His Asn Ile Val Leu		
530	535	540
Lys Arg Glu Leu Gly Glu Gly Ala Phe Gly Lys Val Phe Leu Ala		
545	550	555
Glu Cys Tyr Asn Leu Cys Pro Glu Gln Asp Lys Ile Leu Val Ala		
560	565	570
Val Lys Thr Leu Lys Asp Ala Ser Asp Asn Ala Arg Lys Asp Phe		
575	580	585
His Arg Glu Ala Glu Leu Leu Thr Asn Leu Gln His Glu His Ile		
590	595	600
Val Lys Phe Tyr Gly Val Cys Val Glu Gly Asp Pro Leu Ile Met		
605	610	615
Val Phe Glu Tyr Met Lys His Gly Asp Leu Asn Lys Phe Leu Arg		
620	625	630
Ala His Gly Pro Asp Ala Val Leu Met Ala Glu Gly Asn Pro Pro		
635	640	645
Thr Glu Leu Thr Gln Ser Gln Met Leu His Ile Ala Gln Gln Ile		
650	655	660
Ala Ala Gly Met Val Tyr Leu Ala Ser Gln His Phe Val His Arg		

665	670	675
Asp Leu Ala Thr Arg Asn Cys Leu Val	Gly Glu Asn Leu Leu Val	
680	685	690
Lys Ile Gly Asp Phe Gly Met Ser Arg	Asp Val Tyr Ser Thr Asp	
695	700	705
Tyr Tyr Arg Val Gly Gly His Thr Met	Leu Pro Ile Arg Trp Met	
710	715	720
Pro Pro Glu Ser Ile Met Tyr Arg Lys	Phe Thr Thr Glu Ser Asp	
725	730	735
Val Trp Ser Leu Gly Val Val Leu Trp	Glu Ile Phe Thr Tyr Gly	
740	745	750
Lys Gln Pro Trp Tyr Gln Leu Ser Asn	Asn Glu Val Ile Glu Cys	
755	760	765
Ile Thr Gln Gly Arg Val Leu Gln Arg	Pro Arg Thr Cys Pro Gln	
770	775	780
Glu Val Tyr Glu Leu Met Leu Gly Cys	Trp Gln Arg Glu Pro His	
785	790	795
Met Arg Lys Asn Ile Lys Gly Ile His	Thr Leu Leu Gln Asn Leu	
800	805	810
Ala Lys Ala Ser Pro Val Tyr Leu Asp	Ile Leu Gly	
815	820	822

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1870 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGAAGGTTTA AAGAAGAAGC CGCAAAGCGC AGGGAAGGCC TCCCGGCACG 50

GGTGGGGGAA AGCGGCCGGT GCAGCGCGGG GACAGGCACT CGGGCTGGCA 100

CTGGCTGCTA GGGATGTCGT CCTGGATAAG GTGGCATGGA CCCGCCATGG 150

CGCGGCTCTG GGGCTTCTGC TGGCTGGTTG TGGGCTTCTG GAGGGCCGCT 200

TTCGCCTGTC CCACGTCCTG CAAATGCAGT GCCTCTCGGA TCTGGTGCAG 250

CGACCCTTCT CCTGGCATCG TGGCATTTCC GAGATTGGAG CCTAACAGTG 300

TAGATCCTGA GAACATCACC GAAATTTTCA TCGCAAACCA GAAAAGGTTA 350



GAAATCATCA ACGAAGATGA TGTGAAGCT TATGTGGGAC TGAGAAATCT 400  
GACAATTGTG GATTCTGGAT TAAAATTTGT GGCTCATAAA GCATTTCTGA 450  
AAAACAGCAA CCTGCAGCAC ATCAATTTTA CCCGAAACAA ACTGACGAGT 500  
TTGTCTAGGA AACATTTCCG TCACCTTGAC TTGTCTGAAC TGATCCTGGT 550  
GGGCAATCCA TTTACATGCT CCTGTGACAT TATGTGGATC AAGACTCTCC 600  
AAGAGGCTAA ATCCAGTCCA GACACTCAGG ATTTGTACTG CCTGAATGAA 650  
AGCAGCAAGA ATATTCCCCT GGCAAACCTG CAGATACCCA ATTGTGGTTT 700  
GCCATCTGCA AATCTGGCCG CACCTAACCT CACTGTGGAG GAAGGAAAGT 750  
CTATCACATT ATCCTGTAGT GTGGCAGGTG ATCCGGTTCC TAATATGTAT 800  
TGGGATGTTG GTAACCTGGT TTCCAAACAT ATGAATGAAA CAAGCCACAC 850  
ACAGGGCTCC TTAAGGATAA CTAACATTTT ATCCGATGAC AGTGGGAAGC 900  
AGATCTCTTG TGTGGCGGAA AATCTTGTAG GAGAAGATCA AGATTCTGTC 950  
AACCTCACTG TGCATTTTGC ACCAACTATC ACATTTCTCG AATCTCCAAC 1000  
CTCAGACCAC CACTGGTGCA TTCCATTAC TGTGAAAGGC AACCCAAAAC 1050  
CAGCGCTTCA GTGGTTCTAT AACGGGGCAA TATTGAATGA GTCCAAATAC 1100  
ATCTGTACTA AAATACATGT TACCAATCAC ACGGAGTACC ACGGCTGCCT 1150  
CCAGCTGGAT AATCCCCTC ACATGAACAA TGGGGACTAC ACTCTAATAG 1200  
CCAAGAATGA GTATGGGAAG GATGAGAAAC AGATTTCTGC TCACTTCATG 1250  
GGCTGGCCTG GAATTGACGA TGGTGCAAAC CCAAATTATC CTGATGTAAT 1300  
TTATGAAGAT TATGGAAGT CAGCGAATGA CATCGGGGAC ACCACGAACA 1350  
GAAGTAATGA AATCCCTTCC ACAGACGTCA CTGATAAAAC CGGTCGGGAA 1400  
CATCTCTCGG TCTATGCTGT GGTGGTGATT GCGTCTGTGG TGGGATTTTG 1450  
CCTTTTGGTA ATGCTGTTTC TGCTTAAGTT GGCAAGACAC TCCAAGTTTG 1500  
GCATGAAAGG TTTTGTGTTG TTTATAAGA TCCCACTGGA TGGGTAGCTG 1550  
AAATAAGGA AAAGACAGAG AAAGGGGCTG TGGTGCTTGT TGGTTGATGC 1600  
TGCCATGTAA GCTGGACTCC TGGGACTGCT GTTGGCTTAT CCCGGAAGT 1650  
GCTGCTTATC TGGGGTTTTT TGGTAGATGT GGGCGGTGTT TGGAGGCTGT 1700  
ACTATATGAA GCCTGCATAT ACTGTGAGCT GTGATTGGGG AACACCAATG 1750  
CAGAGGTAAC TCTCAGGCAG CTAAGCAGCA CCTCAAGAAA ACATGTTAAA 1800

TTAATGCTTC TCTTCTTACA GTAGTTCAAA TACAAAAC TG AAATGAAATC 1850

CCATTGGATT GTACTTCTCT 1870

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ser	Ser	Trp	Ile	Arg	Trp	His	Gly	Pro	Ala	Met	Ala	Arg	Leu	
1				5					10					15	
Trp	Gly	Phe	Cys	Trp	Leu	Val	Val	Gly	Phe	Trp	Arg	Ala	Ala	Phe	
				20					25					30	
Ala	Cys	Pro	Thr	Ser	Cys	Lys	Cys	Ser	Ala	Ser	Arg	Ile	Trp	Cys	
				35					40					45	
Ser	Asp	Pro	Ser	Pro	Gly	Ile	Val	Ala	Phe	Pro	Arg	Leu	Glu	Pro	
				50					55					60	
Asn	Ser	Val	Asp	Pro	Glu	Asn	Ile	Thr	Glu	Ile	Phe	Ile	Ala	Asn	
				65					70					75	
Gln	Lys	Arg	Leu	Glu	Ile	Ile	Asn	Glu	Asp	Asp	Val	Glu	Ala	Tyr	
				80					85					90	
Val	Gly	Leu	Arg	Asn	Leu	Thr	Ile	Val	Asp	Ser	Gly	Leu	Lys	Phe	
				95					100					105	
Val	Ala	His	Lys	Ala	Phe	Leu	Lys	Asn	Ser	Asn	Leu	Gln	His	Ile	
				110					115					120	
Asn	Phe	Thr	Arg	Asn	Lys	Leu	Thr	Ser	Leu	Ser	Arg	Lys	His	Phe	
				125					130					135	
Arg	His	Leu	Asp	Leu	Ser	Glu	Leu	Ile	Leu	Val	Gly	Asn	Pro	Phe	
				140					145					150	
Thr	Cys	Ser	Cys	Asp	Ile	Met	Trp	Ile	Lys	Thr	Leu	Gln	Glu	Ala	
				155					160					165	
Lys	Ser	Ser	Pro	Asp	Thr	Gln	Asp	Leu	Tyr	Cys	Leu	Asn	Glu	Ser	
				170					175					180	
Ser	Lys	Asn	Ile	Pro	Leu	Ala	Asn	Leu	Gln	Ile	Pro	Asn	Cys	Gly	
				185					190					195	
Leu	Pro	Ser	Ala	Asn	Leu	Ala	Ala	Pro	Asn	Leu	Thr	Val	Glu	Glu	
				200					205					210	
Gly	Lys	Ser	Ile	Thr	Leu	Ser	Cys	Ser	Val	Ala	Gly	Asp	Pro	Val	

215	220	225
Pro Asn Met Tyr Trp Asp Val Gly Asn	Leu Val Ser Lys His Met	
230	235	240
Asn Glu Thr Ser His Thr Gln Gly Ser	Leu Arg Ile Thr Asn Ile	
245	250	255
Ser Ser Asp Asp Ser Gly Lys Gln Ile	Ser Cys Val Ala Glu Asn	
260	265	270
Leu Val Gly Glu Asp Gln Asp Ser Val	Asn Leu Thr Val His Phe	
275	280	285
Ala Pro Thr Ile Thr Phe Leu Glu Ser	Pro Thr Ser Asp His His	
290	295	300
Trp Cys Ile Pro Phe Thr Val Lys Gly	Asn Pro Lys Pro Ala Leu	
305	310	315
Gln Trp Phe Tyr Asn Gly Ala Ile Leu	Asn Glu Ser Lys Tyr Ile	
320	325	330
Cys Thr Lys Ile His Val Thr Asn His	Thr Glu Tyr His Gly Cys	
335	340	345
Leu Gln Leu Asp Asn Pro Thr His Met	Asn Asn Gly Asp Tyr Thr	
350	355	360
Leu Ile Ala Lys Asn Glu Tyr Gly Lys	Asp Glu Lys Gln Ile Ser	
365	370	375
Ala His Phe Met Gly Trp Pro Gly Ile	Asp Asp Gly Ala Asn Pro	
380	385	390
Asn Tyr Pro Asp Val Ile Tyr Glu Asp	Tyr Gly Thr Ala Ala Asn	
395	400	405
Asp Ile Gly Asp Thr Thr Asn Arg Ser	Asn Glu Ile Pro Ser Thr	
410	415	420
Asp Val Thr Asp Lys Thr Gly Arg Glu	His Leu Ser Val Tyr Ala	
425	430	435
Val Val Val Ile Ala Ser Val Val Gly	Phe Cys Leu Leu Val Met	
440	445	450
Leu Phe Leu Leu Lys Leu Ala Arg His	Ser Lys Phe Gly Met Lys	
455	460	465
Gly Phe Val Leu Phe His Lys Ile Pro	Leu Asp Gly	
470	475	477

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2715 base pairs

(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGATCCGCGT CGGAGATGGA TGTCTCTCTT TGCCCAGCCA AGTGTAGTTT 50  
CTGGCGGATT TTCTTGCTGG GAAGCGTCTG GCTGGACTAT GTGGGCTCCG 100  
TGCTGGCTTG CCCTGCAAAT TGTGTCTGCA GCAAGACTGA GATCAATTGC 150  
CGGCGGCCGG ACGATGGGAA CCTCTTCCCC CTCCTGGAAG GGCAGGATTC 200  
AGGGAACAGC AATGGGAACG CCAATATCAA CATCACGGAC ATCTCAAGGA 250  
ATATCACTTC CATAACATA GAGAACTGGC GCAGTCTTCA CACGCTCAAC 300  
GCCGTGGACA TGGAGCTCTA CACCGGACTT CAAAAGCTGA CCATCAAGAA 350  
CTCAGGACTT CGGAGCATTG AGCCCAGAGC CTTTGCCAAG AACCCCCATT 400  
TGCGTTATAT AAACCTGTCA AGTAACCGGC TCACCACACT CTCGTGGCAG 450  
CTCTTCCAGA CGCTGAGTCT TCGGGAATTG CAGTTGGAGC AGAACTTTTT 500  
CAACTGCAGC TGTGACATCC GCTGGATGCA GCTCTGGCAG GAGCAGGGGG 550  
AGGCCAAGCT CAACAGCCAG AACCTCTACT GCATCAATGC TGATGGCTCC 600  
CAGCTTCCTC TCTTCCGCAT GAACATCAGT CAGTGTGACC TTCCTGAGAT 650  
CAGCGTGAGC CACGTCAACC TGACCGTACG AGAGGGTGAC AATGCTGTTA 700  
TCACTTGCAA TGGCTCTGGA TCACCCCTTC CTGATGTGGA CTGGATAGTC 750  
ACTGGGCTGC AGTCCATCAA CACTCACCAG ACCAATCTGA ACTGGACCAA 800  
TGTTGATGCC ATCAACTTGA CGCTGGTGAA TGTGACGAGT GAGGACAATG 850  
GCTTACCCTT GACGTGCATT GCAGAGAACG TGGTGGGCAT GAGCAATGCC 900  
AGTGTGCCCC TCACTGTCTA CTATCCCCCA CGTGTGGTGA GCCTGGAGGA 950  
GCCTGAGCTG CGCCTGGAGC ACTGCATCGA GTTTGTGGTG CGTGGCAACC 1000  
CCCCACCAAC GCTGCACTGG CTGCACAATG GGCAGCCTCT GCGGGAGTCC 1050  
AAGATCATCC ATGTGGAATA CTACCAAGAG GGAGAGATTT CCGAGGGCTG 1100  
CCTGCTCTTC AACAAGCCCA CCCACTACAA CAATGGCAAC TATACCCTCA 1150  
TTGCCAAAAA CCCACTGGGC ACAGCCAACC AGACCATCAA TGGCCACTTC 1200  
CTCAAGGAGC CCTTTCCAGA GAGCACGGAT AACTTTATCT TGTTTGACGA 1250

AGTGAGTCCC ACACCTCCTA TCACTGTGAC CCACAAACCA GAAGAAGACA 1300  
 CTTTTGGGGT ATCCATAGCA GTTGGACTTG CTGCTTTTGC CTGTGTCCTG 1350  
 TTGGTGGTTC TCTTCGTCAT GATCAACAAA TATGGTCGAC GGTCCAAATT 1400  
 TGGAATGAAG GGTCCCGTGG CTGTCATCAG TGGTGAGGAG GACTCAGCCA 1450  
 GCCCCTGCA CCACATCAAC CACGGCATCA CCACGCCCTC GTCCTGGAT 1500  
 GCGGGGCCCCG AACTGTGGT CATTGGCATG ACTCGCATCC CTGTCATTGA 1550  
 GAACCCCCAG TACTTCCGTC AGGGACACAA CTGCCACAAG CCGGACACGT 1600  
 ATGTGCAGCA CATTAAAGAG AGAGACATCG TGCTGAAGCG AGAACTGGGT 1650  
 GAGGGAGCCT TTGGAAAGGT CTTCTGGCC GAGTGCTACA ACCTCAGCCC 1700  
 GACCAAGGAC AAGATGCTTG TGGCTGTGAA GGCCCTGAAG GATCCCACCC 1750  
 TGGCTGCCCCG GAAGGATTTT CAGAGGGAGG CCGAGCTGCT CACCAACCTG 1800  
 CAGCATGAGC ACATTGTCAA GTTCTATGGA GTGTGCGGCG ATGGGGACCC 1850  
 CCTCATCATG GTCTTTGAAT ACATGAAGCA TGGAGACCTG AATAAGTTCC 1900  
 TCAGGGCCCA TGGGCCAGAT GCAATGATCC TTGTGGATGG ACAGCCACGC 1950  
 CAGGCCAAGG GTGAGCTGGG GCTCTCCCAA ATGCTCCACA TTGCCAGTCA 2000  
 GATCGCCTCG GGTATGGTGT ACCTGGCCTC CCAGCACTTT GTGCACCGAG 2050  
 ACCTGGCCAC CAGGAACTGC CTGGTTGGAG CGAATCTGCT AGTGAAGATT 2100  
 GGGGACTTCG GCATGTCCAG AGATGTCTAC AGCACGGATT ATTACAGGCT 2150  
 CTTTAATCCA TCTGGAAATG ATTTTGTAT ATGGTGTGAG GTGGGAGGAC 2200  
 ACACCATGCT CCCCATTGCG TGGATGCCTC CTGAAAGCAT CATGTACCGG 2250  
 AAGTTCAC TA CAGAGAGTGA TGTATGGAGC TTCGGGGTGA TCCTCTGGGA 2300  
 GATCTTCACC TATGGAAAGC AGCCATGGTT CCAACTCTCA AACACGGAGG 2350  
 TCATTGAGTG CATTACCCAA GGTCGTGTTT TGGAGCGGCC CCGAGTCTGC 2400  
 CCCAAAGAGG TGTACGATGT CATGCTGGGG TGCTGGCAGA GGGAACCACA 2450  
 GCAGCGGTTG AACATCAAGG AGATCTACAA AATCCTCCAT GCTTTGGGGA 2500  
 AGGCCACCCC AATCTACCTG GACATTCTTG GCTAGTGGTG GCTGGTGGTC 2550  
 ATGAATTCAT ACTCTGTTGC CTCCTCTCTC CCTGCCTCAC ATCTCCCTTC 2600  
 CACCTCACAA CTCCTTCCAT CCTTGACTGA AGCGAACATC TTCATATAAA 2650  
 CTCAAGTGCC TGCTACACAT ACAACACTGA AAAAAGGAAA AAAAAAGAAA 2700

AAAAAAAAAA ACCGC 2715

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 839 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Asp	Val	Ser	Leu	Cys	Pro	Ala	Lys	Cys	Ser	Phe	Trp	Arg	Ile	
1				5					10					15	
Phe	Leu	Leu	Gly	Ser	Val	Trp	Leu	Asp	Tyr	Val	Gly	Ser	Val	Leu	
				20					25					30	
Ala	Cys	Pro	Ala	Asn	Cys	Val	Cys	Ser	Lys	Thr	Glu	Ile	Asn	Cys	
				35					40					45	
Arg	Arg	Pro	Asp	Asp	Gly	Asn	Leu	Phe	Pro	Leu	Leu	Glu	Gly	Gln	
				50					55					60	
Asp	Ser	Gly	Asn	Ser	Asn	Gly	Asn	Ala	Asn	Ile	Asn	Ile	Thr	Asp	
				65					70					75	
Ile	Ser	Arg	Asn	Ile	Thr	Ser	Ile	His	Ile	Glu	Asn	Trp	Arg	Ser	
				80					85					90	
Leu	His	Thr	Leu	Asn	Ala	Val	Asp	Met	Glu	Leu	Tyr	Thr	Gly	Leu	
				95					100					105	
Gln	Lys	Leu	Thr	Ile	Lys	Asn	Ser	Gly	Leu	Arg	Ser	Ile	Gln	Pro	
				110					115					120	
Arg	Ala	Phe	Ala	Lys	Asn	Pro	His	Leu	Arg	Tyr	Ile	Asn	Leu	Ser	
				125					130					135	
Ser	Asn	Arg	Leu	Thr	Thr	Leu	Ser	Trp	Gln	Leu	Phe	Gln	Thr	Leu	
				140					145					150	
Ser	Leu	Arg	Glu	Leu	Gln	Leu	Glu	Gln	Asn	Phe	Phe	Asn	Cys	Ser	
				155					160					165	
Cys	Asp	Ile	Arg	Trp	Met	Gln	Leu	Trp	Gln	Glu	Gln	Gly	Glu	Ala	
				170					175					180	
Lys	Leu	Asn	Ser	Gln	Asn	Leu	Tyr	Cys	Ile	Asn	Ala	Asp	Gly	Ser	
				185					190					195	
Gln	Leu	Pro	Leu	Phe	Arg	Met	Asn	Ile	Ser	Gln	Cys	Asp	Leu	Pro	
				200					205					210	
Glu	Ile	Ser	Val	Ser	His	Val	Asn	Leu	Thr	Val	Arg	Glu	Gly	Asp	
				215					220					225	

Asn Ala Val Ile Thr Cys Asn Gly Ser	Gly Ser Pro Leu Pro Asp	230	235	240
Val Asp Trp Ile Val Thr Gly Leu Gln Ser Ile Asn Thr His Gln		245	250	255
Thr Asn Leu Asn Trp Thr Asn Val His Ala Ile Asn Leu Thr Leu		260	265	270
Val Asn Val Thr Ser Glu Asp Asn Gly Phe Thr Leu Thr Cys Ile		275	280	285
Ala Glu Asn Val Val Gly Met Ser Asn Ala Ser Val Ala Leu Thr		290	295	300
Val Tyr Tyr Pro Pro Arg Val Val Ser Leu Glu Glu Pro Glu Leu		305	310	315
Arg Leu Glu His Cys Ile Glu Phe Val Val Arg Gly Asn Pro Pro		320	325	330
Pro Thr Leu His Trp Leu His Asn Gly Gln Pro Leu Arg Glu Ser		335	340	345
Lys Ile Ile His Val Glu Tyr Tyr Gln Glu Gly Glu Ile Ser Glu		350	355	360
Gly Cys Leu Leu Phe Asn Lys Pro Thr His Tyr Asn Asn Gly Asn		365	370	375
Tyr Thr Leu Ile Ala Lys Asn Pro Leu Gly Thr Ala Asn Gln Thr		380	385	390
Ile Asn Gly His Phe Leu Lys Glu Pro Phe Pro Glu Ser Thr Asp		395	400	405
Asn Phe Ile Leu Phe Asp Glu Val Ser Pro Thr Pro Pro Ile Thr		410	415	420
Val Thr His Lys Pro Glu Glu Asp Thr Phe Gly Val Ser Ile Ala		425	430	435
Val Gly Leu Ala Ala Phe Ala Cys Val Leu Leu Val Val Leu Phe		440	445	450
Val Met Ile Asn Lys Tyr Gly Arg Arg Ser Lys Phe Gly Met Lys		455	460	465
Gly Pro Val Ala Val Ile Ser Gly Glu Glu Asp Ser Ala Ser Pro		470	475	480
Leu His His Ile Asn His Gly Ile Thr Thr Pro Ser Ser Leu Asp		485	490	495
Ala Gly Pro Asp Thr Val Val Ile Gly Met Thr Arg Ile Pro Val		500	505	510

Ile	Glu	Asn	Pro	Gln	Tyr	Phe	Arg	Gln	Gly	His	Asn	Cys	His	Lys	
				515					520					525	
Pro	Asp	Thr	Tyr	Val	Gln	His	Ile	Lys	Arg	Arg	Asp	Ile	Val	Leu	
				530					535					540	
Lys	Arg	Glu	Leu	Gly	Glu	Gly	Ala	Phe	Gly	Lys	Val	Phe	Leu	Ala	
				545					550					555	
Glu	Cys	Tyr	Asn	Leu	Ser	Pro	Thr	Lys	Asp	Lys	Met	Leu	Val	Ala	
				560					565					570	
Val	Lys	Ala	Leu	Lys	Asp	Pro	Thr	Leu	Ala	Ala	Arg	Lys	Asp	Phe	
				575					580					585	
Gln	Arg	Glu	Ala	Glu	Leu	Leu	Thr	Asn	Leu	Gln	His	Glu	His	Ile	
				590					595					600	
Val	Lys	Phe	Tyr	Gly	Val	Cys	Gly	Asp	Gly	Asp	Pro	Leu	Ile	Met	
				605					610					615	
Val	Phe	Glu	Tyr	Met	Lys	His	Gly	Asp	Leu	Asn	Lys	Phe	Leu	Arg	
				620					625					630	
Ala	His	Gly	Pro	Asp	Ala	Met	Ile	Leu	Val	Asp	Gly	Gln	Pro	Arg	
				635					640					645	
Gln	Ala	Lys	Gly	Glu	Leu	Gly	Leu	Ser	Gln	Met	Leu	His	Ile	Ala	
				650					655					660	
Ser	Gln	Ile	Ala	Ser	Gly	Met	Val	Tyr	Leu	Ala	Ser	Gln	His	Phe	
				665					670					675	
Val	His	Arg	Asp	Leu	Ala	Thr	Arg	Asn	Cys	Leu	Val	Gly	Ala	Asn	
				680					685					690	
Leu	Leu	Val	Lys	Ile	Gly	Asp	Phe	Gly	Met	Ser	Arg	Asp	Val	Tyr	
				695					700					705	
Ser	Thr	Asp	Tyr	Tyr	Arg	Leu	Phe	Asn	Pro	Ser	Gly	Asn	Asp	Phe	
				710					715					720	
Cys	Ile	Trp	Cys	Glu	Val	Gly	Gly	His	Thr	Met	Leu	Pro	Ile	Arg	
				725					730					735	
Trp	Met	Pro	Pro	Glu	Ser	Ile	Met	Tyr	Arg	Lys	Phe	Thr	Thr	Glu	
				740					745					750	
Ser	Asp	Val	Trp	Ser	Phe	Gly	Val	Ile	Leu	Trp	Glu	Ile	Phe	Thr	
				755					760					765	
Tyr	Gly	Lys	Gln	Pro	Trp	Phe	Gln	Leu	Ser	Asn	Thr	Glu	Val	Ile	
				770					775					780	
Glu	Cys	Ile	Thr	Gln	Gly	Arg	Val	Leu	Glu	Arg	Pro	Arg	Val	Cys	
				785					790					795	



Pro Lys Glu Val Tyr Asp Val Met Leu Gly Cys Trp Gln Arg Glu  
800 805 810

Pro Gln Gln Arg Leu Asn Ile Lys Glu Ile Tyr Lys Ile Leu His  
815 820 825

Ala Leu Gly Lys Ala Thr Pro Ile Tyr Leu Asp Ile Leu Gly  
830 835 839

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1858 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGATCCGCGT CGGAGATGGA TGTCTCTCTT TGCCCAGCCA AGTGTAGTTT 50  
CTGGCGGATT TTCTTGCTGG GAAGCGTCTG GCTGGACTAT GTGGGCTCCG 100  
TGCTGGCTTG CCCTGCAAAT TGTGTCTGCA GCAAGACTGA GATCAATTGC 150  
CGGCGGCCCG ACGATGGGAA CCTCTTCCCC CTCCTGGAAG GGCAGGATTC 200  
AGGGAACAGC AATGGGAACG CCAATATCAA CATCACGGAC ATCTCAAGGA 250  
ATATCACTTC CATAACATA GAGAACTGGC GCAGTCTTCA CACGCTCAAC 300  
GCCGTGGACA TGGAGCTCTA CACCGGACTT CAAAAGCTGA CCATCAAGAA 350  
CTCAGGACTT CGGAGCATTC AGCCCAGAGC CTTTGCCAAG AACCCCCATT 400  
TGCGTTATAT AAACCTGTCA AGTAACCGGC TCACCACACT CTCGTGGCAG 450  
CTCTTCCAGA CGCTGAGTCT TCGGGAATTG CAGTTGGAGC AGAACTTTTT 500  
CAACTGCAGC TGTGACATCC GCTGGATGCA GCTCTGGCAG GAGCAGGGGG 550  
AGGCCAAGCT CAACAGCCAG AACCTCTACT GCATCAATGC TGATGGCTCC 600  
CAGCTTCCTC TCTTCCGCAT GAACATCAGT CAGTGTGACC TTCCTGAGAT 650  
CAGCGTGAGC CACGTCAACC TGACCGTACG AGAGGGTGAC AATGCTGTTA 700  
TCACTTGCAA TGGCTCTGGA TCACCCCTTC CTGATGTGGA CTGGATAGTC 750  
ACTGGGCTGC AGTCCATCAA CACTCACCAG ACCAATCTGA ACTGGACCAA 800  
TGTTTCATGCC ATCAACTTGA CGCTGGTGAA TGTGACGAGT GAGGACAATG 850  
GCTTCACCCT GACGTGCATT GCAGAGAACG TGGTGGGCAT GAGCAATGCC 900  
AGTGTGCCCC TCACTGTCTA CTATCCCCCA CGTGTGGTGA GCCTGGAGGA 950

GCCTGAGCTG CGCCTGGAGC ACTGCATCGA GTTTGTGGTG CGTGGCAACC 1000  
 CCCCACCAAC GCTGCACTGG CTGCACAATG GGCAGCCTCT GCGGGAGTCC 1050  
 AAGATCATCC ATGTGGAATA CTACCAAGAG GGAGAGATTT CCGAGGGCTG 1100  
 CCTGCTCTTC AACAAGCCCA CCCACTACAA CAATGGCAAC TATACCCTCA 1150  
 TTGCCAAAAA CCCACTGGGC ACAGCCAACC AGACCATCAA TGGCCACTTC 1200  
 CTCAAGGAGC CCTTTCCAGA GAGCACGGAT AACTTTATCT TGTTTGACGA 1250  
 AGTGAGTCCC ACACCTCCTA TCACTGTGAC CCACAAACCA GAAGAAGACA 1300  
 CTTTTGGGGT ATCCATAGCA GTTGGACTTG CTGCTTTTGC CTGTGTCCTG 1350  
 TTGGTGGTTC TCTTCGTCAT GATCAACAAA TATGGTCGAC GGTCCAAATT 1400  
 TGGAATGAAG GGTCCCGTGG CTGTCATCAG TGGTGAGGAG GACTCAGCCA 1450  
 GCCCACTGCA CCACATCAAC CACGGCATCA CCACGCCCTC GTCACTGGAT 1500  
 GCCGGGCCCCG AACTGTGGT CATTGGCATG ACTCGCATCC CTGTCATTGA 1550  
 GAACCCCCAG TACTTCCGTC AGGGACACAA CTGCCACAAG CCGGACACGT 1600  
 GGGTCTTTTC AAACATAGAC AATCATGGGA TATTAACTT GAAGGACAAT 1650  
 AGAGATCATC TAGTCCCATC AACTCACTAT ATATATGAGG AACCTGAGGT 1700  
 CCAGAGTGGG GAAGTGTCTT ACCCAAGGTC ACATGGTTTC AGAGAAATTA 1750  
 TGTGAATCC AATAAGCCTT CCCGGACATT CCAAGCCTCT TAACCATGGC 1800  
 ATCTATGTTG AGGATGTCAA TGTTTATTTT AGCAAAGGAC GTCATGGCCT 1850  
 TTAAAAAC 1858

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 612 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Asp	Val	Ser	Leu	Cys	Pro	Ala	Lys	Cys	Ser	Phe	Trp	Arg	Ile
1				5				10						15
Phe	Leu	Leu	Gly	Ser	Val	Trp	Leu	Asp	Tyr	Val	Gly	Ser	Val	Leu
			20					25						30
Ala	Cys	Pro	Ala	Asn	Cys	Val	Cys	Ser	Lys	Thr	Glu	Ile	Asn	Cys
			35					40						45



Pro Thr Leu His Trp Leu His Asn Gly Gln Pro Leu Arg Glu Ser	335	340	345
Lys Ile Ile His Val Glu Tyr Tyr Gln Glu Gly Glu Ile Ser Glu	350	355	360
Gly Cys Leu Leu Phe Asn Lys Pro Thr His Tyr Asn Asn Gly Asn	365	370	375
Tyr Thr Leu Ile Ala Lys Asn Pro Leu Gly Thr Ala Asn Gln Thr	380	385	390
Ile Asn Gly His Phe Leu Lys Glu Pro Phe Pro Glu Ser Thr Asp	395	400	405
Asn Phe Ile Leu Phe Asp Glu Val Ser Pro Thr Pro Pro Ile Thr	410	415	420
Val Thr His Lys Pro Glu Glu Asp Thr Phe Gly Val Ser Ile Ala	425	430	435
Val Gly Leu Ala Ala Phe Ala Cys Val Leu Leu Val Val Leu Phe	440	445	450
Val Met Ile Asn Lys Tyr Gly Arg Arg Ser Lys Phe Gly Met Lys	455	460	465
Gly Pro Val Ala Val Ile Ser Gly Glu Glu Asp Ser Ala Ser Pro	470	475	480
Leu His His Ile Asn His Gly Ile Thr Thr Pro Ser Ser Leu Asp	485	490	495
Ala Gly Pro Asp Thr Val Val Ile Gly Met Thr Arg Ile Pro Val	500	505	510
Ile Glu Asn Pro Gln Tyr Phe Arg Gln Gly His Asn Cys His Lys	515	520	525
Pro Asp Thr Trp Val Phe Ser Asn Ile Asp Asn His Gly Ile Leu	530	535	540
Asn Leu Lys Asp Asn Arg Asp His Leu Val Pro Ser Thr His Tyr	545	550	555
Ile Tyr Glu Glu Pro Glu Val Gln Ser Gly Glu Val Ser Tyr Pro	560	565	570
Arg Ser His Gly Phe Arg Glu Ile Met Leu Asn Pro Ile Ser Leu	575	580	585
Pro Gly His Ser Lys Pro Leu Asn His Gly Ile Tyr Val Glu Asp	590	595	600
Val Asn Val Tyr Phe Ser Lys Gly Arg His Gly Phe	605	610	612

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Leu	Arg	Gly	Gly	Arg	Arg	Gly	Gln	Leu	Gly	Trp	His	Ser	Trp	1	5	10	15
Ala	Ala	Gly	Pro	Gly	Ser	Leu	Leu	Ala	Trp	Leu	Ile	Leu	Ala	Ser	20	25	30	
Ala	Gly	Ala	Ala	Pro	Cys	Pro	Asp	Ala	Cys	Cys	Pro	His	Gly	Ser	35	40	45	
Ser	Gly	Leu	Arg	Cys	Thr	Arg	Asp	Gly	Ala	Leu	Asp	Ser	Leu	His	50	55	60	
His	Leu	Pro	Gly	Ala	Glu	Asn	Leu	Thr	Glu	Leu	Tyr	Ile	Glu	Asn	65	70	75	
Gln	Gln	His	Leu	Gln	His	Leu	Glu	Leu	Arg	Asp	Leu	Arg	Gly	Leu	80	85	90	
Gly	Glu	Leu	Arg	Asn	Leu	Thr	Ile	Val	Lys	Ser	Gly	Leu	Arg	Phe	95	100	105	
Val	Ala	Pro	Asp	Ala	Phe	His	Phe	Thr	Pro	Arg	Leu	Ser	Arg	Leu	110	115	120	
Asn	Leu	Ser	Phe	Asn	Ala	Leu	Glu	Ser	Leu	Ser	Trp	Lys	Thr	Val	125	130	135	
Gln	Gly	Leu	Ser	Leu	Gln	Glu	Leu	Val	Leu	Ser	Gly	Asn	Pro	Leu	140	145	150	
His	Cys	Ser	Cys	Ala	Leu	Arg	Trp	Leu	Gln	Arg	Trp	Glu	Glu	Glu	155	160	165	
Gly	Leu	Gly	Gly	Val	Pro	Glu	Gln	Lys	Leu	Gln	Cys	His	Gly	Gln	170	175	180	
Gly	Pro	Leu	Ala	His	Met	Pro	Asn	Ala	Ser	Cys	Gly	Val	Pro	Thr	185	190	195	
Leu	Lys	Val	Gln	Val	Pro	Asn	Ala	Ser	Val	Asp	Val	Gly	Asp	Asp	200	205	210	
Val	Leu	Leu	Arg	Cys	Gln	Val	Glu	Gly	Arg	Gly	Leu	Glu	Gln	Ala	215	220	225	
Gly	Trp	Ile	Leu	Thr	Glu	Leu	Glu	Gln	Ser	Ala	Thr	Val	Met	Lys	230	235	240	

Ser Gly Gly Leu Pro Ser Leu Gly Leu Thr Leu Ala Asn Val Thr	245	250	255
Ser Asp Leu Asn Arg Lys Asn Leu Thr Cys Trp Ala Glu Asn Asp	260	265	270
Val Gly Arg Ala Glu Val Ser Val Gln Val Asn Val Ser Phe Pro	275	280	285
Ala Ser Val Gln Leu His Thr Ala Val Glu Met His His Trp Cys	290	295	300
Ile Pro Phe Ser Val Asp Gly Gln Pro Ala Pro Ser Leu Arg Trp	305	310	315
Leu Phe Asn Gly Ser Val Leu Asn Glu Thr Ser Phe Ile Phe Thr	320	325	330
Glu Phe Leu Glu Pro Ala Ala Asn Glu Thr Val Arg His Gly Cys	335	340	345
Leu Arg Leu Asn Gln Pro Thr His Val Asn Asn Gly Asn Tyr Thr	350	355	360
Leu Leu Ala Ala Asn Pro Phe Gly Gln Ala Ser Ala Ser Ile Met	365	370	375
Ala Ala Phe Met Asp Asn Pro Phe Glu Phe Asn Pro Glu Asp Pro	380	385	390
Ile Pro Asp Thr Asn Ser Thr Ser Gly Asp Pro Val Glu Lys Lys	395	400	405
Asp Glu Thr Pro Phe Gly Val Ser Val Ala Val Gly Leu Ala Val	410	415	420
Phe Ala Cys Leu Phe Leu Ser Thr Leu Leu Leu Val Leu Asn Lys	425	430	435
Cys Gly Arg Arg Asn Lys Phe Gly Ile Asn Arg Pro Ala Val Leu	440	445	450
Ala Pro Glu Asp Gly Leu Ala Met Ser Leu His Phe Met Thr Leu	455	460	465
Gly Gly Ser Ser Leu Ser Pro Thr Glu Gly Lys Gly Ser Gly Leu	470	475	480
Gln Gly His Ile Ile Glu Asn Pro Gln Tyr Phe Ser Asp Ala Cys	485	490	495
Val His His Ile Lys Arg Arg Asp Ile Val Leu Lys Trp Glu Leu	500	505	510
Gly Glu Gly Ala Phe Gly Lys Val Phe Leu Ala Glu Cys His Asn	515	520	525



- (A) LENGTH: 23 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGYGAYATHA TGTGGYTNAAC 23

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGGATGCARY TNTGGCARCA RCA 23

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

YTCRTCYYTN CCRTAYTCRT T 21

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCYTCYTGRY ARTAYTCNAC GTG 23

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CACGTCAACA ACGGCAACTA CA 22

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGAAGGATGA GAAACAGATT TCTGC 25

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CATCAATGGC CACTTCCTCA AGG 23

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGGTGTTTCG TCCTTCTTCT CC 22

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAGATGTGCC CGACCGGTTG TATC 24

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CACAGTGATA GGAGGTGTGG GA 22

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGATGTGGCT CCAGGCCCC 19

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGGCAACCCG CCCACGGAA 19

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACGCCAGGCC AAGGGTGAG 19

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: Nucleic Acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TAACCACTCC CAGCCCCTGG 20

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTGGTGGCCT CCAGCGGCAG 20

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AATTCATGAC CACCAGCCAC CA 22

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCTCCTCGGG ACTGCGATGC 20

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGTCGCCCT GGCCGAGGTG GCAT 24

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAGCTCAACA GCCAGAACCT C 21

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAGCTCTGTG AGGATCCAGC C 21

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCGACCGGTT TTATCAGTGA C 21

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGATCTTGG ACTCCCGCAG AGG 23

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTTGCCAAG GCATCTCCGG T 21

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGTGCAGCA CATTAAGAGG A 21

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TTATACACAG GCTTAAGCCA TCCA 24

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGGAGGCATC CAGCGAATG 19

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Glu Ser Thr Asp Asn Phe Ile Leu Phe  
1 5 9

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Leu Phe Asn Pro Ser Gly Asn Asp Phe Cys Ile Trp Cys Glu  
1 5 10 14

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TCTCCTTCTC GCCGGTGG 18

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ser Pro Ser Arg Arg Trp  
1 5 6

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Phe Val Leu Phe His Lys Ile Pro Leu Asp Gly  
1 5 10 11

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Trp	Val	Phe	Ser	Asn	Ile	Asp	Asn	His	Gly	Ile	Leu	Asn	Leu	Lys
1				5					10					15
Asp	Asn	Arg	Asp	His	Leu	Val	Pro	Ser	Thr	His	Tyr	Ile	Tyr	Glu
				20					25					30
Glu	Pro	Glu	Val	Gln	Ser	Gly	Glu	Val	Ser	Tyr	Pro	Arg	Ser	His
				35					40					45
Gly	Phe	Arg	Glu	Ile	Met	Leu	Asn	Pro	Ile	Ser	Leu	Pro	Gly	His
				50					55					60
Ser	Lys	Pro	Leu	Asn	His	Gly	Ile	Tyr	Val	Glu	Asp	Val	Asn	Val
				65					70					75
Tyr	Phe	Ser	Lys	Gly	Arg	His	Gly	Phe						
				80				84						

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